

FIGURE 1A

SEQ ID NO:04	*	*	*****	*	*****	***	
SEQ ID NO:10	MEALS-----						
SEQ ID NO:20	MEG-----						
SEQ ID NO:22	MESH-----						
SEQ ID NO:24	MKVHQFARGF--WEHEPSLTIGCKRLRPLAKLSNTDTISPPHPEVTFDLKSFIKPSAS						
SEQ ID NO:25	MKVHQFTRGLIWEHEPFLTIGCKRLRPLAKLPNTKITTP-----FDLKSFIKPSGP						
	MEPPQHQH-----HHH-----						
	1						60
SEQ ID NO:04	**	*	*****	*	*****	*	
SEQ ID NO:10	-----G-----RVGYKC-----						
SEQ ID NO:20	-----SDAEENVRTHSSV-----						
SEQ ID NO:22	RKLIGSSDDNTNKRDPSSPQQAETHIPGTRWNPTQEQIGILEMILY-RGGMRTPNAQQ						
SEQ ID NO:24	RK-----PVSSDDTKDPSPQQLETH-PGTRWNPTQEQIGILEMILY-RGGMRTPNAQQ						
SEQ ID NO:25	-----QADQESGNNNKGSGGYTCR-QTSTRWPTTEQIKILKELYNNNAIRSPTAQQ						
	61						120
SEQ ID NO:04	*	*	*****	*	*	*	
SEQ ID NO:10	IQRISTHLSAFGKVESKNVYFWFQNHKARERHHK-KRRRGASSSSPDSGSGRGSNNNEED						
SEQ ID NO:20	TVRIKLLERFAGVDANVYFWFQNRSRRRQRQLQAQAAASSSSSGSPPTSGLAPGH						
SEQ ID NO:22	IQOITSLRAYGHIEGKNVYFWFQNHKAROKLM-KOOTIAYSNR----FLASHFICQ						
SEQ ID NO:24	IEQITAOQLSKYGKIEGKNVYFWFQNHKARERQKQ--KRNNLGLAHSPTTLTTSPPFSC-						
SEQ ID NO:25	IEQITVQLGKYGKIEGKNVYFWFQNHKARERQKQ--KRSSLASHSPRTTIHS-----						
	IQKITARLRFQKIEGKNVYFWFQNHKARERQKRENGTNNMTTPSSSPNSVMMAANDHYH						
	121						180

FIGURE 1B (CONTINUED from 1A)

SEQ ID NO:04	---	GRGAASQSHDAD-ADADLVLOPPESKREARS-YG--HHHRL-----	*	*	
SEQ ID NO:10	SEQ ID NO:20	ATASSTAGMFAHGATYGSSASAPFPFSCGMMGDLDDYGGDDLFAISRQMGYASGGGS			
SEQ ID NO:22	SEQ ID NO:24	---NVACAPYCLQ---RSGFSFYPOQSKVLAAGGIS--STGPL-----			
SEQ ID NO:25		---CVITIMDTT-KRGEVV---ERE-EEDSPLK-K-CR-----			
		---VVITLTT--RGEVV---ERDHEEDSPYK--KKCR-----			
		PLLHHHGVPMQRPANSVNVKLNQDHHLYHHNKPYPFNNGNLHASSGTECGVNASN			240
		181			
			*	*	
SEQ ID NO:04	SEQ ID NO:10	--VTCYVRDVVEQQ-----EASPSWERPTRE-----VETLELFLPKSYGDLE--A			
SEQ ID NO:20	SEQ ID NO:22	GSASSAAVAHEHQOQLYYSP-----CQPASMTVFINGVATEVPRGPIDLRSMF			
SEQ ID NO:24	SEQ ID NO:25	--G--MORMFDM-----QSS--EHPDCN-----REVLTFLPLHPTGILKEKT			
		---SWAFYLEDQ-----R-----EE-E-----HRTLELFLPLHEG-----			
		---RWYFDCLEQ-----NMSGPCQE-E-----HRTLELFLPLHEG-----			
		GYNSSHYGSMEOQDCSMNYYNNGGGMNDHHYSSAPYNFDRAKPLFGLGEGHDEECG			300
		241			
			*	*	
SEQ ID NO:04	SEQ ID NO:10	AEKVRSVVRGIA---ATS---ECCRELS---FFDVSAGRDP-----LELRICSGFP			
SEQ ID NO:20	SEQ ID NO:22	QDQVMLVHSTAGLPLVNEYGVLTSQLMGESYF-----LVTRGY			
SEQ ID NO:24	SEQ ID NO:25	THQVPSLASTSV---VAV---DEDGLGNQPPFNFTTEPRS---RE-----R			
		-----R-----			
		GDVLEHRRRTLPLPFMHG---EDHINGSGAIWKYQSEVVRPCASLELR-----N			
		301			356